

- 1 -

piece 1, NC_000913, fur_REPO64+, config: linear, direction: +, begin: 709840, end: 710150

5' *709840 * *709850 * *709860 * *709870 * *709880 * *709890 * *709900 * *709910 * *709920 3'

- phe - leu - -

- phe - phe - arg - ala - val - leu - leu - ser - val - met - arg - asn - leu - ser - cys - tyr - -

- ser - leu - gly - arg - tyr - cys - tyr - gln - ser - cys - gly - ile - cys - pro - val - thr - lys - arg - phe - thr - ser - leu - glu - glu - val - thr - glu -

... -----] NC_000913.fur ... sd

{-----} sd-(6)-ir 709938 Gap 4.3 bits

|-----| sd-ir 709938 fur_REPO64+ total 6.5 bits

3.8 Bits } p35-(22)-p10 709947 Gap 2.3 bits
p35-p10 709947 total 5.7 bits

p35 4.6 bits

} p35-(21)-p10 709952 Gap 3.3 bits
p35-p10 709952 total 7.9 bits

p35-p10_709993 total 4.6 bits

p35 4.7 bits

1

{-----} ... p35-(25)-p10 710022 Gap

The figure shows a tRNA precursor with various processing sites indicated by red dots. The mature tRNA sequence is shown below the precursor, with amino acid assignments (e.g., lysine, serine, valine) and codon positions (e.g., *710010, *710020). Three predicted folding regions are highlighted: p10 (5.1 bits), p35 (5.0 bits), and p10 (2.7 bits). These regions are represented by colored boxes (red, green, blue) indicating different structural contexts or domains.

... -----] p35-(25)-p10 710022 Gap 4.0 bits